

10/554561

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SEQUENCE LISTING

<110> YOUSUKE, EBINA  
TOSHIYUKI, OBATA  
MEDICAL AND BIOLOGICAL LABORATORIES CO., LTD.

<120> METHOD FOR DETERMINATION OF INSULIN RECEPTOR ALPHA SUBUNIT

<130> M3-A0301Y1P

<150> JP 2003-121955  
<151> 2003-04-25

<150> JP 2003-433303  
<151> 2003-12-26

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<170> PatentIn version 3.1

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10/554561

## SEQUENCE LISTING

<110> Ebina, Yousuke  
Obata, Toshiyuki  
Okamoto, Eiji

JC20 Rec'd PCT/PTO 25 OCT 2005

<120> METHODS FOR MEASURING THE INSULIN  
RECEPTOR ALPHA SUBUNIT

<130> 082368-006600US

<150> PCT/JP2004/005412

<151> 2004-04-15

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Val Ile His Asn Asn Lys Cys Ile Pro Glu Cys Pro Ser Gly Tyr Thr	
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atg aat tcc agc aac ttg ctg tgc acc cca tgc ctg ggt ccc tgt ccc	1008

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Tyr	Ala	Leu	Val	Ser	Leu	Ser	Phe	Phe	Arg	Lys	Leu	Arg	Leu	Ile	Arg		
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gga	gag	acc	ttg	gaa	att	ggg	aac	tac	tcc	ttc	tat	gcc	ttg	gac	aac	1296	
Gly	Glu	Thr	Leu	Glu	Ile	Gly	Asn	Tyr	Ser	Phe	Tyr	Ala	Leu	Asp	Asn		
390					395					400					405		
cag	aac	cta	agg	cag	ctc	tgg	gac	tgg	agc	aaa	cac	aac	ctc	acc	acc	1344	
Gln	Asn	Leu	Arg	Gln	Leu	Trp	Asp	Trp	Ser	Lys	His	Asn	Leu	Thr	Thr		
				410					415					420			
act	cag	ggg	aaa	ctc	ttc	ttc	cac	tat	aac	ccc	aaa	ctc	tgc	ttg	tca	1392	
Thr	Gln	Gly	Lys	Leu	Phe	Phe	His	Tyr	Asn	Pro	Lys	Leu	Cys	Leu	Ser		
			425					430					435				
gaa	atc	cac	aag	atg	gaa	gaa	gtt	tca	gga	acc	aag	ggg	cgc	cag	gag	1440	
Glu	Ile	His	Lys	Met	Glu	Glu	Val	Ser	Gly	Thr	Lys	Gly	Arg	Gln	Glu		
		440					445					450					
aga	aac	gac	att	gcc	ctg	aag	acc	aat	ggg	gac	aag	gca	tcc	tgt	gaa	1488	
Arg	Asn	Asp	Ile	Ala	Leu	Lys	Thr	Asn	Gly	Asp	Lys	Ala	Ser	Cys	Glu		
		455				460					465						
aat	gag	tta	ctt	aaa	ttt	tct	tac	att	cgg	aca	tct	ttt	gac	aag	atc	1536	
Asn	Glu	Leu	Leu	Lys	Phe	Ser	Tyr	Ile	Arg	Thr	Ser	Phe	Asp	Lys	Ile		
470					475					480					485		
ttg	ctg	aga	tgg	gag	ccg	tac	tgg	ccc	ccc	gac	ttc	cga	gac	ctc	ttg	1584	
Leu	Leu	Arg	Trp	Glu	Pro	Tyr	Trp	Pro	Pro	Asp	Phe	Arg	Asp	Leu	Leu		
				490					495					500			
ggg	ttc	atg	ctg	ttc	tac	aaa	gag	gcc	cct	tat	cag	aat	gtg	acg	gag	1632	
Gly	Phe	Met	Leu	Phe	Tyr	Lys	Glu	Ala	Pro	Tyr	Gln	Asn	Val	Thr	Glu		
			505					510					515				
ttc	gat	ggg	cag	gat	gcg	tgt	ggc	tcc	aac	agt	tgg	acg	gtg	gta	gac	1680	
Phe	Asp	Gly	Gln	Asp	Ala	Cys	Gly	Ser	Asn	Ser	Trp	Thr	Val	Val	Asp		
		520					525					530					
att	gac	cca	ccc	ctg	agg	tcc	aac	gac	ccc	aaa	tca	cag	aac	cac	cca	1728	
Ile	Asp	Pro	Pro	Leu	Arg	Ser	Asn	Asp	Pro	Lys	Ser	Gln	Asn	His	Pro		



535	540	545	
ggg tgg ctg atg cgg ggt ctc aag ccc tgg acc cag tat gcc atc ttt Gly Trp Leu Met Arg Gly Leu Lys Pro Trp Thr Gln Tyr Ala Ile Phe 550 555 560 565			1776
gtg aag acc ctg gtc acc ttt tcg gat gaa cgc cgg acc tat ggg gcc Val Lys Thr Leu Val Thr Phe Ser Asp Glu Arg Arg Thr Tyr Gly Ala 570 575 580			1824
aag agt gac atc att tat gtc cag aca gat gcc acc aac ccc tct gtg Lys Ser Asp Ile Ile Tyr Val Gln Thr Asp Ala Thr Asn Pro Ser Val 585 590 595			1872
ccc ctg gat cca atc tca gtg tct aac tca tca tcc cag att att ctg Pro Leu Asp Pro Ile Ser Val Ser Asn Ser Ser Ser Gln Ile Ile Leu 600 605 610			1920
aag tgg aaa cca ccc tcc gac ccc aat ggc aac atc acc cac tac ctg Lys Trp Lys Pro Pro Ser Asp Pro Asn Gly Asn Ile Thr His Tyr Leu 615 620 625			1968
gtt ttc tgg gag agg cag gcg gaa gac agt gag ctg ttc gag ctg gat Val Phe Trp Glu Arg Gln Ala Glu Asp Ser Glu Leu Phe Glu Leu Asp 630 635 640 645			2016
tat tgc ctc aaa ggg ctg aag ctg ccc tcg agg acc tgg tct cca cca Tyr Cys Leu Lys Gly Leu Lys Leu Pro Ser Arg Thr Trp Ser Pro Pro 650 655 660			2064
ttc gag tct gaa gat tct cag aag cac aac cag agt gag tat gag gat Phe Glu Ser Glu Asp Ser Gln Lys His Asn Gln Ser Glu Tyr Glu Asp 665 670 675			2112
tcg gcc ggc gaa tgc tgc tcc tgt cca aag aca gac tct cag atc ctg Ser Ala Gly Glu Cys Cys Ser Cys Pro Lys Thr Asp Ser Gln Ile Leu 680 685 690			2160
aag gag ctg gag gag tcc tcg ttt agg aag acg ttt gag gat tac ctg Lys Glu Leu Glu Glu Ser Ser Phe Arg Lys Thr Phe Glu Asp Tyr Leu 695 700 705			2208
cac aac gtg gtt ttc gtc ccc aga aaa acc tct tca ggc act ggt gcc His Asn Val Val Phe Val Pro Arg Lys Thr Ser Ser Gly Thr Gly Ala 710 715 720 725			2256
gag gac cct agg cca tct cgg aaa cgc agg tcc ctt ggc gat gtt ggg Glu Asp Pro Arg Pro Ser Arg Lys Arg Arg Ser Leu Gly Asp Val Gly 730 735 740			2304
aat gtg acg gtg gcc gtg ccc acg gtg gca gct ttc ccc aac act tcc Asn Val Thr Val Ala Val Pro Thr Val Ala Ala Phe Pro Asn Thr Ser 745 750 755			2352
tcg acc agc gtg ccc acg agt ccg gag gag cac agg cct ttt gag aag Ser Thr Ser Val Pro Thr Ser Pro Glu Glu His Arg Pro Phe Glu Lys 760 765 770			2400
gtg gtg aac aag gag tcg ctg gtc atc tcc ggc ttg cga cac ttc acg Val Val Asn Lys Glu Ser Leu Val Ile Ser Gly Leu Arg His Phe Thr			2448

775	780	785	
ggc tat cgc atc gag ctg cag gct tgc aac cag gac acc cct gag gaa			2496
Gly Tyr Arg Ile Glu Leu Gln Ala Cys Asn Gln Asp Thr Pro Glu Glu			
790	795	800	805
cgg tgc agt gtg gca gcc tac gtc agt gcg agg acc atg cct gaa gcc			2544
Arg Cys Ser Val Ala Ala Tyr Val Ser Ala Arg Thr Met Pro Glu Ala			
	810	815	820
aag gct gat gac att gtt ggc cct gtg acg cat gaa atc ttt gag aac			2592
Lys Ala Asp Asp Ile Val Gly Pro Val Thr His Glu Ile Phe Glu Asn			
	825	830	835
aac gtc gtc cac ttg atg tgg cag gag ccg aag gag ccc aat ggt ctg			2640
Asn Val Val His Leu Met Trp Gln Glu Pro Lys Glu Pro Asn Gly Leu			
	840	845	850
atc gtg ctg tat gaa gtg agt tat cgg cga tat ggt gat gag gag ctg			2688
Ile Val Leu Tyr Glu Val Ser Tyr Arg Arg Tyr Gly Asp Glu Glu Leu			
	855	860	865
cat ctc tgc gtc tcc cgc aag cac ttc gct ctg gaa cgg ggc tgc agg			2736
His Leu Cys Val Ser Arg Lys His Phe Ala Leu Glu Arg Gly Cys Arg			
	870	875	880
ctg cgt ggg ctg tca ccg ggg aac tac agc gtg cga atc cgg gcc acc			2784
Leu Arg Gly Leu Ser Pro Gly Asn Tyr Ser Val Arg Ile Arg Ala Thr			
	890	895	900
tcc ctt gcg ggc aac ggc tct tgg acg gaa ccc acc tat ttc tac gtg			2832
Ser Leu Ala Gly Asn Gly Ser Trp Thr Glu Pro Thr Tyr Phe Tyr Val			
	905	910	915
aca gac tat tta gac gtc ccg tca aat			2859
Thr Asp Tyr Leu Asp Val Pro Ser Asn			
	920	925	
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	-25	-20	-15
Ala Val Ala Ala Leu Leu Leu Gly Ala Ala Gly His Leu Tyr Pro Gly			
	-10	-5	1
Glu Val Cys Pro Gly Met Asp Ile Arg Asn Asn Leu Thr Arg Leu His			
	10	15	20
Glu Leu Glu Asn Cys Ser Val Ile Glu Gly His Leu Gln Ile Leu Leu			
	25	30	35
Met Phe Lys Thr Arg Pro Glu Asp Phe Arg Asp Leu Ser Phe Pro Lys			
	40	45	50
Leu Ile Met Ile Thr Asp Tyr Leu Leu Leu Phe Arg Val Tyr Gly Leu			

55	60	65
Glu Ser Leu Lys Asp Leu Phe Pro Asn Leu Thr Val Ile Arg Gly Ser		
70	75	80
Arg Leu Phe Phe Asn Tyr Ala Leu Val Ile Phe Glu Met Val His Leu		
	90	95
Lys Glu Leu Gly Leu Tyr Asn Leu Met Asn Ile Thr Arg Gly Ser Val		
	105	110
Arg Ile Glu Lys Asn Asn Glu Leu Cys Tyr Leu Ala Thr Ile Asp Trp		
	120	125
Ser Arg Ile Leu Asp Ser Val Glu Asp Asn His Ile Val Leu Asn Lys		
	135	140
Asp Asp Asn Glu Glu Cys Gly Asp Ile Cys Pro Gly Thr Ala Lys Gly		
150	155	160
Lys Thr Asn Cys Pro Ala Thr Val Ile Asn Gly Gln Phe Val Glu Arg		
	170	175
Cys Trp Thr His Ser His Cys Gln Lys Val Cys Pro Thr Ile Cys Lys		
	185	190
Ser His Gly Cys Thr Ala Glu Gly Leu Cys Cys His Ser Glu Cys Leu		
	200	205
Gly Asn Cys Ser Gln Pro Asp Asp Pro Thr Lys Cys Val Ala Cys Arg		
	215	220
Asn Phe Tyr Leu Asp Gly Arg Cys Val Glu Thr Cys Pro Pro Pro Tyr		
230	235	240
Tyr His Phe Gln Asp Trp Arg Cys Val Asn Phe Ser Phe Cys Gln Asp		
	250	255
Leu His His Lys Cys Lys Asn Ser Arg Arg Gln Gly Cys His Gln Tyr		
	265	270
Val Ile His Asn Asn Lys Cys Ile Pro Glu Cys Pro Ser Gly Tyr Thr		
	280	285
Met Asn Ser Ser Asn Leu Leu Cys Thr Pro Cys Leu Gly Pro Cys Pro		
	295	300
Lys Val Cys His Leu Leu Glu Gly Glu Lys Thr Ile Asp Ser Val Thr		
310	315	320
Ser Ala Gln Glu Leu Arg Gly Cys Thr Val Ile Asn Gly Ser Leu Ile		
	330	335
Ile Asn Ile Arg Gly Gly Asn Asn Leu Ala Ala Glu Leu Glu Ala Asn		
	345	350
Leu Gly Leu Ile Glu Glu Ile Ser Gly Tyr Leu Lys Ile Arg Arg Ser		
	360	365
Tyr Ala Leu Val Ser Leu Ser Phe Phe Arg Lys Leu Arg Leu Ile Arg		
	375	380
Gly Glu Thr Leu Glu Ile Gly Asn Tyr Ser Phe Tyr Ala Leu Asp Asn		
390	395	400
Gln Asn Leu Arg Gln Leu Trp Asp Trp Ser Lys His Asn Leu Thr Thr		
	410	415
Thr Gln Gly Lys Leu Phe Phe His Tyr Asn Pro Lys Leu Cys Leu Ser		
	425	430
Glu Ile His Lys Met Glu Glu Val Ser Gly Thr Lys Gly Arg Gln Glu		
	440	445
Arg Asn Asp Ile Ala Leu Lys Thr Asn Gly Asp Lys Ala Ser Cys Glu		
	455	460
Asn Glu Leu Leu Lys Phe Ser Tyr Ile Arg Thr Ser Phe Asp Lys Ile		
470	475	480
Leu Leu Arg Trp Glu Pro Tyr Trp Pro Pro Asp Phe Arg Asp Leu Leu		
	490	495
Gly Phe Met Leu Phe Tyr Lys Glu Ala Pro Tyr Gln Asn Val Thr Glu		
	505	510
Phe Asp Gly Gln Asp Ala Cys Gly Ser Asn Ser Trp Thr Val Val Asp		
	520	525
Ile Asp Pro Pro Leu Arg Ser Asn Asp Pro Lys Ser Gln Asn His Pro		
535	540	545

Gly	Trp	Leu	Met	Arg	Gly	Leu	Lys	Pro	Trp	Thr	Gln	Tyr	Ala	Ile	Phe
550					555					560					565
Val	Lys	Thr	Leu	Val	Thr	Phe	Ser	Asp	Glu	Arg	Arg	Thr	Tyr	Gly	Ala
				570					575						580
Lys	Ser	Asp	Ile	Ile	Tyr	Val	Gln	Thr	Asp	Ala	Thr	Asn	Pro	Ser	Val
			585					590					595		
Pro	Leu	Asp	Pro	Ile	Ser	Val	Ser	Asn	Ser	Ser	Ser	Gln	Ile	Ile	Leu
		600					605					610			
Lys	Trp	Lys	Pro	Pro	Ser	Asp	Pro	Asn	Gly	Asn	Ile	Thr	His	Tyr	Leu
	615					620					625				
Val	Phe	Trp	Glu	Arg	Gln	Ala	Glu	Asp	Ser	Glu	Leu	Phe	Glu	Leu	Asp
630					635					640					645
Tyr	Cys	Leu	Lys	Gly	Leu	Lys	Leu	Pro	Ser	Arg	Thr	Trp	Ser	Pro	Pro
				650					655					660	
Phe	Glu	Ser	Glu	Asp	Ser	Gln	Lys	His	Asn	Gln	Ser	Glu	Tyr	Glu	Asp
			665					670					675		
Ser	Ala	Gly	Glu	Cys	Cys	Ser	Cys	Pro	Lys	Thr	Asp	Ser	Gln	Ile	Leu
		680					685					690			
Lys	Glu	Leu	Glu	Glu	Ser	Ser	Phe	Arg	Lys	Thr	Phe	Glu	Asp	Tyr	Leu
	695					700					705				
His	Asn	Val	Val	Phe	Val	Pro	Arg	Lys	Thr	Ser	Ser	Gly	Thr	Gly	Ala
710					715					720					725
Glu	Asp	Pro	Arg	Pro	Ser	Arg	Lys	Arg	Arg	Ser	Leu	Gly	Asp	Val	Gly
				730					735					740	
Asn	Val	Thr	Val	Ala	Val	Pro	Thr	Val	Ala	Ala	Phe	Pro	Asn	Thr	Ser
			745					750					755		
Ser	Thr	Ser	Val	Pro	Thr	Ser	Pro	Glu	Glu	His	Arg	Pro	Phe	Glu	Lys
		760					765					770			
Val	Val	Asn	Lys	Glu	Ser	Leu	Val	Ile	Ser	Gly	Leu	Arg	His	Phe	Thr
	775					780					785				
Gly	Tyr	Arg	Ile	Glu	Leu	Gln	Ala	Cys	Asn	Gln	Asp	Thr	Pro	Glu	Glu
790					795					800					805
Arg	Cys	Ser	Val	Ala	Ala	Tyr	Val	Ser	Ala	Arg	Thr	Met	Pro	Glu	Ala
				810					815					820	
Lys	Ala	Asp	Asp	Ile	Val	Gly	Pro	Val	Thr	His	Glu	Ile	Phe	Glu	Asn
			825					830					835		
Asn	Val	Val	His	Leu	Met	Trp	Gln	Glu	Pro	Lys	Glu	Pro	Asn	Gly	Leu
		840					845					850			
Ile	Val	Leu	Tyr	Glu	Val	Ser	Tyr	Arg	Arg	Tyr	Gly	Asp	Glu	Glu	Leu
	855					860					865				
His	Leu	Cys	Val	Ser	Arg	Lys	His	Phe	Ala	Leu	Glu	Arg	Gly	Cys	Arg
870					875					880					885
Leu	Arg	Gly	Leu	Ser	Pro	Gly	Asn	Tyr	Ser	Val	Arg	Ile	Arg	Ala	Thr
				890					895					900	
Ser	Leu	Ala	Gly	Asn	Gly	Ser	Trp	Thr	Glu	Pro	Thr	Tyr	Phe	Tyr	Val
			905					910					915		
Thr	Asp	Tyr	Leu	Asp	Val	Pro	Ser	Asn							
		920					925								